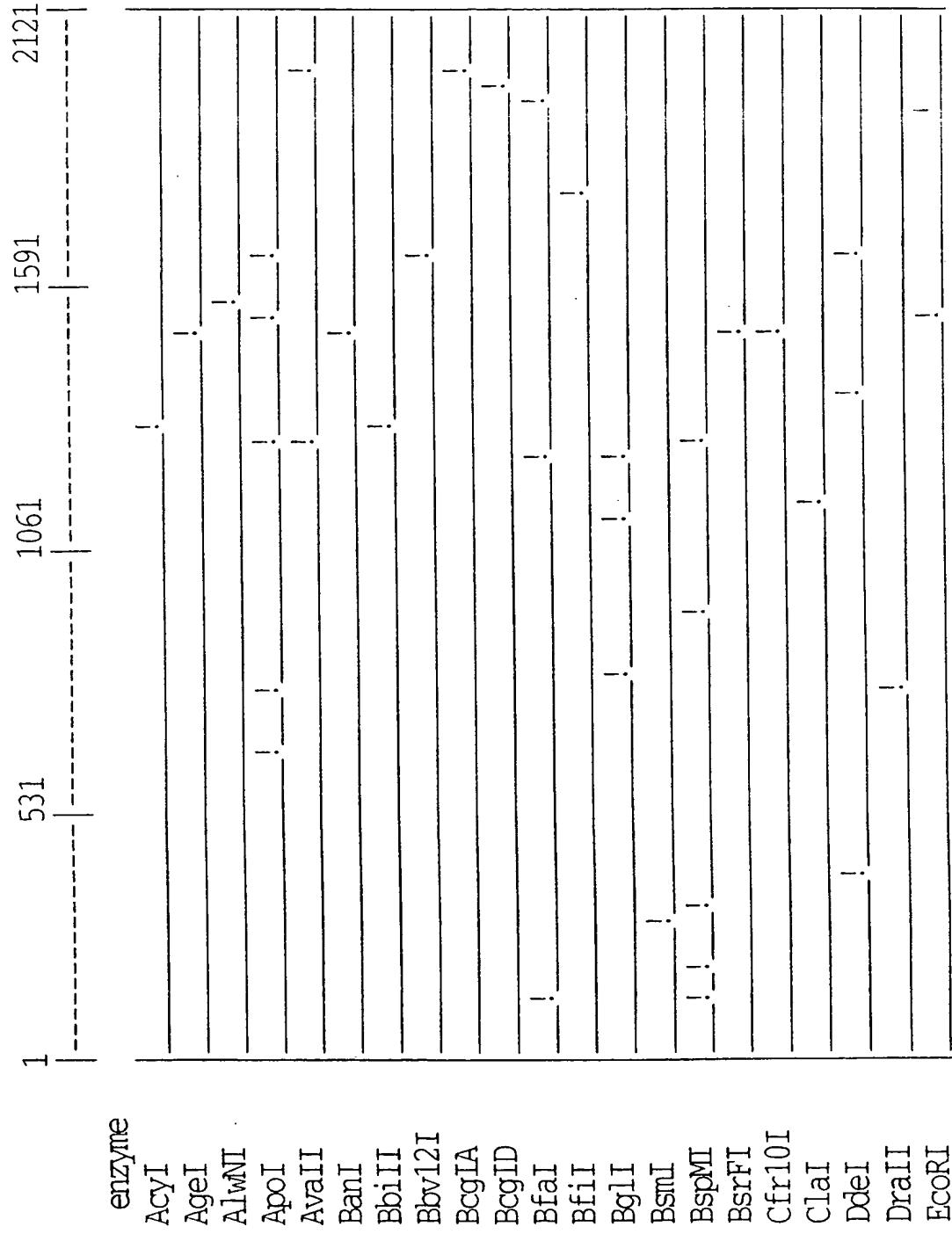


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FIG. 1A

Restriction map of *M. catarrhalis* strain MB5 *tbpB* gene

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FIG. 1B

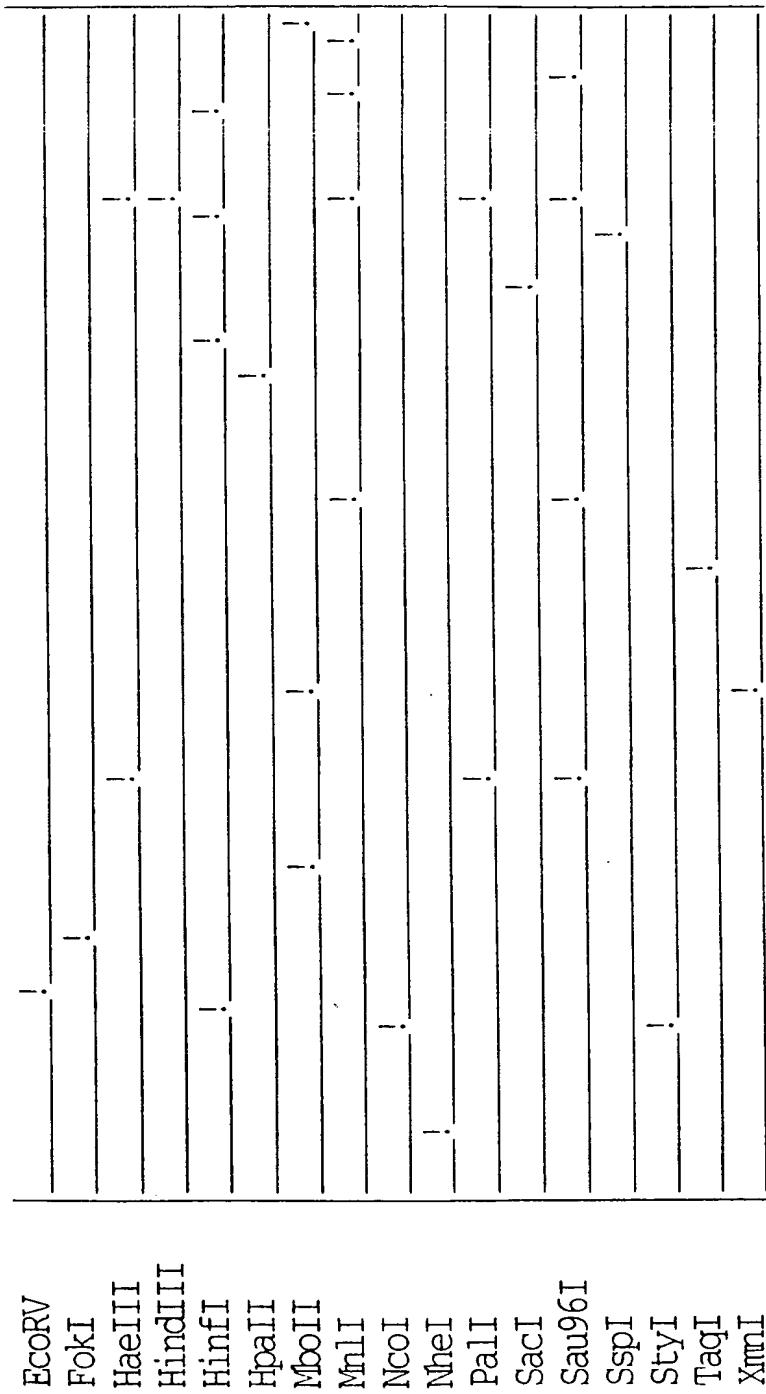


FIG. 2A

M. catarrhalis strain MB5 *tbpB* sequence

FIG.2B

ASP	VAL	PRO	THR	ASP	GLU	ASN	LYS	ASP	...	
G A T G T G C C A A C C G A T G A A A A T A A A A G A T ...										
250	260	270	280	290	300					
GLY	TYR	GLY	MET	ALA	LEU	SER	LYS	MET	ASN	...
G G T T A T G G C A T G G C T T G A G T A A A A T G A A T ...										
310	320	330	340	350	360	373				
GLU	LYS	ASP	ILE	ILE	THR	LEU	ASP	GLY	LYS	...
G A A A A A G A T A T C A T T A C C T T A G A C G G T A A A ...										
370	380	390	400	410	420					
LEU	PRO	PHE	SER	LEU	ASP	VAL	GLU	ASN	LYS	...
T T G C C A T T T C G T T G G A T G T A G A A A A T A A A ...										
430	440	450	460	470	480					

FIG.2C

GLU ALA ASP LYS ASN ALA ILE GLY ASP ARG ...
G A A G C G G A T A A A A T G C C A T T G G T G A C A G A ...
490 500 510 ...
... ILE LYS ASP ASN LYS ASP LYS SER LEU
... A T T A A G A A A G A T A A T A A G A C A A G T C A T T A
520 530 540 ...

SER LYS ALA GLU LEU ALA LYS GIN ILE LYS ...
T C T A A A G C A G A G C T T G C C A A A C A A T C A A A ...
550 560 570 ...
... GLU ASP VAL ARG LYS SER HIS GLU PHE GIN 5/73
... G A A G A T G T G C G T A A A A G C C A T G A G T T C A G 3
580 590 600 ...

GIN VAL LEU SER SER LEU LYS ASN LYS ILE ...
C A A G T A T T A T C A C T G A A A A A A T T ...
610 620 630 ...
... PHE HIS SER ASN ASP GLY THR LYS AIA
... T T T C A T T C A A A T G A T G G A A C A A C C A A A G C A
640 650 660 ...

THR THR ARG ASP LEU GIN TIR VAL ASP TYR
A C C A C A C G A G A T T A C A A T A T G T T G A T T A T
670 680 690 ...
... GLY TYR TYR LEU VAL ASN ASP GLY ASN TYR
... G G T T A C T A C T T G G T G A A T G A T T G C A A T T A T
710 720 ...

FIG.2D

LEU	THR	VAL	LYS	THR	ASP	GLU	LEU	TRP	ASN	...
C T : A C C G T C A A A C A G A C G A C T T T G G A A T										
730	740	750								
	LEU	GLY	PRO	VAL	GLY	GLY	VAL	PHE
			TTA G G C C C T G T G G C G G T G T G T T A T A T			TYR	ASN
						760	770			
						780				
GLY	THR	THR	THR	ALA	LYS	GLU	LEU	PRO	THR	...
G G C A C A A C G A C C G C C A A A G A G C T A C C C A C A...										
790	800	810...								
	GLN	ASP	ALA	VAL	LYS	TYR	LYS	GLY
			HIS
				CAA G A T G C G G T C A A A T A T A A G G A C A T T G G						TRP
				820	830	840	850	860	870...	6/73
ASP	PHE	MET	THR	ASP	VAL	ALA	LYS	GLN	ARG	...
G A C T T T A T G A C C G A T T G T T G C C A A A C A A A G A...										
850	860	870...								
	ASN	ARG	PHE	SER	GLU	VAL	LYS	GLU
			ASN
				AA C C G A T T A G C G A A G T G A A G A A A A C C T T						LEU
				880	890	900	910	920	930...	
GLN	ALA	GLY	ARG	TYR	TYR	GLY	ALA	SER	SER	...
C A : G C A G G T C G G T A T T A T G G A G C A T C T T C A...										
910	920	930...								
	LYS	ASP	GLU	TYR	ASN	ARG	LEU	THR
			ASP
				AA A G A T G A A T A C A A C C G C T T A T A C T G A T						
				940	950	960				

FIG. 2E

GLU LYS ASN LYS PRO GLU ARG TYR ASN GLY ...
 G A G A A A C A A C C A G A G C G T T A T A A C G G T ...
 990 ...
 980 ...
 970 ...
 960 ...
 950 ...
 940 ...
 930 ...
 920 ...
 910 ...
 900 ...
 890 ...
 880 ...
 870 ...
 860 ...
 850 ...
 840 ...
 830 ...
 820 ...
 810 ...
 800 ...
 790 ...
 780 ...
 770 ...
 760 ...
 750 ...
 740 ...
 730 ...
 720 ...
 710 ...
 700 ...
 690 ...
 680 ...
 670 ...
 660 ...
 650 ...
 640 ...
 630 ...
 620 ...
 610 ...
 600 ...
 590 ...
 580 ...
 570 ...
 560 ...
 550 ...
 540 ...
 530 ...
 520 ...
 510 ...
 500 ...
 490 ...
 480 ...
 470 ...
 460 ...
 450 ...
 440 ...
 430 ...
 420 ...
 410 ...
 400 ...
 390 ...
 380 ...
 370 ...
 360 ...
 350 ...
 340 ...
 330 ...
 320 ...
 310 ...
 300 ...
 290 ...
 280 ...
 270 ...
 260 ...
 250 ...
 240 ...
 230 ...
 220 ...
 210 ...
 200 ...
 190 ...
 180 ...
 170 ...
 160 ...
 150 ...
 140 ...
 130 ...
 120 ...
 110 ...
 100 ...
 90 ...
 80 ...
 70 ...
 60 ...
 50 ...
 40 ...
 30 ...
 20 ...
 10 ...
 0 ...

 ASN PHE LYS ASP LYS LYS LEU THR GLY GLU ...
 A A T T T A A G G A C A A A A A A T T A A C A G G T G A G ...
 1050 ...
 1040 ...
 1030 ...
 1020 ...
 1010 ...
 1000 ...
 990 ...
 980 ...
 970 ...
 960 ...
 950 ...
 940 ...
 930 ...
 920 ...
 910 ...
 900 ...
 890 ...
 880 ...
 870 ...
 860 ...
 850 ...
 840 ...
 830 ...
 820 ...
 810 ...
 800 ...
 790 ...
 780 ...
 770 ...
 760 ...
 750 ...
 740 ...
 730 ...
 720 ...
 710 ...
 700 ...
 690 ...
 680 ...
 670 ...
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 610 ...
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 510 ...
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 490 ...
 480 ...
 470 ...
 460 ...
 450 ...
 440 ...
 430 ...
 420 ...
 410 ...
 400 ...
 390 ...
 380 ...
 370 ...
 360 ...
 350 ...
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 330 ...
 320 ...
 310 ...
 300 ...
 290 ...
 280 ...
 270 ...
 260 ...
 250 ...
 240 ...
 230 ...
 220 ...
 210 ...
 200 ...
 190 ...
 180 ...
 170 ...
 160 ...
 150 ...
 140 ...
 130 ...
 120 ...
 110 ...
 100 ...
 90 ...
 80 ...
 70 ...
 60 ...
 50 ...
 40 ...
 30 ...
 20 ...
 10 ...
 0 ...

 GLY ASN VAL THR LYS THR LYS ARG TYR ASP ...
 G G C A A T G T T A C G A A A C C A A A C G C T A T G A C ...
 1110 ...
 1100 ...
 1090 ...
 1080 ...
 1070 ...
 1060 ...
 1050 ...
 1040 ...
 1030 ...
 1020 ...
 1010 ...
 1000 ...
 990 ...
 980 ...
 970 ...
 960 ...
 950 ...
 940 ...
 930 ...
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 880 ...
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 830 ...
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 790 ...
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 540 ...
 530 ...
 520 ...
 510 ...
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 490 ...
 480 ...
 470 ...
 460 ...
 450 ...
 440 ...
 430 ...
 420 ...
 410 ...
 400 ...
 390 ...
 380 ...
 370 ...
 360 ...
 350 ...
 340 ...
 330 ...
 320 ...
 310 ...
 300 ...
 290 ...
 280 ...
 270 ...
 260 ...
 250 ...
 240 ...
 230 ...
 220 ...
 210 ...
 200 ...
 190 ...
 180 ...
 170 ...
 160 ...
 150 ...
 140 ...
 130 ...
 120 ...
 110 ...
 100 ...
 90 ...
 80 ...
 70 ...
 60 ...
 50 ...
 40 ...
 30 ...
 20 ...
 10 ...
 0 ...

 ARG GLY SER ALA THR ALA SER ASP LYS ALA ...
 C G T G G C A G T G C C A C C C G C A A G C A A G C A ...
 1170 ...
 1160 ...
 1150 ...
 1140 ...
 1130 ...
 1120 ...
 1110 ...
 1100 ...
 1090 ...
 1080 ...
 1070 ...
 1060 ...
 1050 ...
 1040 ...
 1030 ...
 1020 ...
 1010 ...
 1000 ...
 990 ...
 980 ...
 970 ...
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 880 ...
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 750 ...
 740 ...
 730 ...
 720 ...
 710 ...
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 690 ...
 680 ...
 670 ...
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 640 ...
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 620 ...
 610 ...
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 520 ...
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 490 ...
 480 ...
 470 ...
 460 ...
 450 ...
 440 ...
 430 ...
 420 ...
 410 ...
 400 ...
 390 ...
 380 ...
 370 ...
 360 ...
 350 ...
 340 ...
 330 ...
 320 ...
 310 ...
 300 ...
 290 ...
 280 ...
 270 ...
 260 ...
 250 ...
 240 ...
 230 ...
 220 ...
 210 ...
 200 ...
 190 ...
 180 ...
 170 ...
 160 ...
 150 ...
 140 ...
 130 ...
 120 ...
 110 ...
 100 ...
 90 ...
 80 ...
 70 ...
 60 ...
 50 ...
 40 ...
 30 ...
 20 ...
 10 ...
 0 ...

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FIG.2F

SER ASP ALA LYS ASN SER LEU GLU GLY GLY ...
 A G C G A T G C C A A A A T A G C C T A G A A G G C G G T ...
 1210 1220 1230 ...
 ... PHE TYR GLY PRO ASN ALA GLU GLU LEU ALA
 ... T T T T A T G G A C C A A A C G C C G A G C T G G C A
 1240 1250 1260 ...

 GLY LYS PHE LEU THR ASN ASP ASN LYS LEU ...
 G G T A A A T T C C T A A C C A A T G A C A A C T C ...
 1270 1280 1290 ...
 ... PHE GLY VAL PHE GLY ALA LYS ARG GLU SER
 ... T T T G G C G T C T T G G T G C T A A A C G A G A G T 8/73
 1300 1310 1320 1330 ...

 LYS ALA GLY GLU LYS THR GLU ALA ILE LEU ...
 A A A G C T G G G G A A A A A C C G A A G C C A T C T T A ...
 1330 1340 1350 ...
 ... ASP ALA TYR ALA LEU GLY THR PHE ASN LYS
 ... G A T G C C T A T G C A C T T G G G A C A T T A A C A A A
 1360 1370 1380 ...

 ASN ASN ALA THR THR PHE THR PRO PHE THR ...
 A A T A A C G C A A C C A C A T T C A C C C A T T A C C ...
 1390 1400 1410 ...
 ... LYS LYS GIN LEU ASP ASN PHE GLY ASN ALA
 ... A A A A A C A A C T G G A T A A C T T G C A A T G C C
 1420 1430 1440 ...

FIG.2G

LYS	LYS	LEU	VAL	LEU	GLY	SER	THR	VAL	ILE	...	
A A A A G T T G G T C T T G G G T T C T A C C G T C A T T...											
1450	1460	1470	1480	1490	1500						
VAL	ASN	GLU	PHE	THR	LYS	ASN	LYS	PRO	ASP	...	
G T C A A T G A A T T C A C C A A A A C A A G C C A G A T...											
1510	1520	1530	1540	1550	1560						
MET	VAL	ASN	ASP	LYS	VAL	SER	VAL	LYS	THR	...	
A T G G T G A A T G A T A A G T T A G C G T C A A A C C...											
1570	1580	1590	1600	1610	1620						
LYS	PHE	GLY	GLU	LEU	SER	VAL	GLY	THR	SER	...	
A A A T T T G G T G A G C T C A G T G T C G G C A C A A G C...											
1630	1640	1650	1660	1670	1680						

FIG.2H

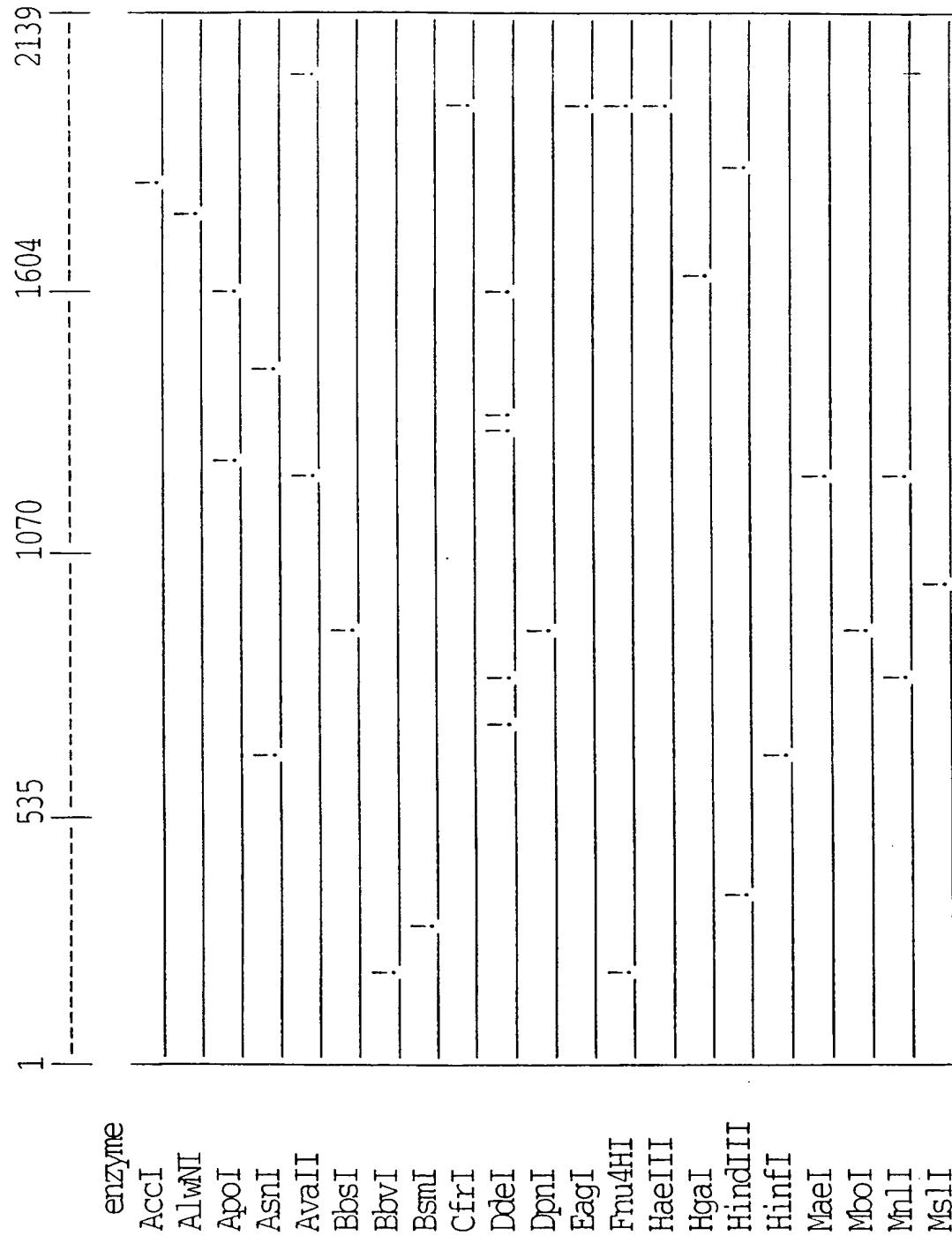
ALA THR THR GLY GLU LYS ALA VAL PRO THR ...
 G C T A C C A C A G G C G A G A A A G C C G T A C C A A C C ...
 1690 1700 1710 ...
 ... LYS GLY THR ALA LYS TYR LEU GLY ASN TRP
 ... A A A G G C A C A G C C A A A T A T T G G G A A C T G G
 1720 1730 1740
 ...
 ...
 VAL GLY TYR ILE THR GLY LYS ASP SER SER ...
 G T A G G A T A C A T C A C A G G A A A G G A C T C A T C A ...
 1750 1760 1770 ...
 ... LYS SER PHE ASN GLU ALA GLN ASP VAL ALA
 ... A A A A G C T T A A T G A G G C C C A A G A T G T T G C T 10 / 73
 1780 1790 1800
 ...
 ...
 ASP PHE ASP ILE ASP PHE GLU LYS SER ...
 G A T T T G A C A T T G A C T T G A G A A A A A T C A ...
 1810 1820 1830 ...
 ... VAL LYS GLY LYS LEU THR THR LYS ASP ARG
 ... G T T A A A G G C A A A C T G A C C A C C A A G A C C G C
 1840 1850 1860
 ...
 ...
 GLN ASP PRO VAL PHE ASN ILE THR GLY ASP ...
 C A A G A C C C T G T A T T A A C A T C A C A G G T G A C ...
 1870 1880 1890 ...
 ... ILE ALA GLY ASN GLY TRP THR GLY LYS ALA
 ... A T C G C A G G C A A T G G C T G G A C A G G C A A A G C C
 1900 1910 1920
 ...

FIG.21

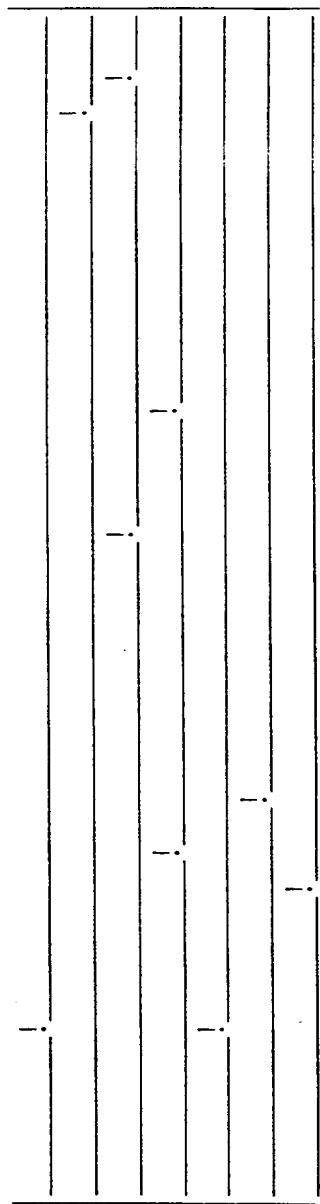
SER	THR	THR	LYS	ALA	ASP	ALA	GLY	GLY	TYR	...
A G C A C C A C C A A G C C G G A C G C A G G G G C T A C...										
1930	1940	1950...	1960	1970	1980	1990	2000	2010...	2020	2030
...	LYS	ILE	ASP	SER	SER	THR	THR	GLY	LYS	SER
...	A A G A T A G A T T C T A G C A G T A C A G G C A A A T C C									
...										
...										
ILE	VAL	ILE	LYS	ASP	ALA	GLU	VAL	THR	GLY	...
A T C G T C A T C A A G A T G C C G A G G T T A C A G G G...										
1990	2000	2010...	2020	2030	2040	2050	2060	2070...	2080	2090
...	GLY	PHE	TYR	GLY	PRO	ASN	ALA	ASN	GLU	MET
...	G G C T T T A T G G T C C A A A T G C A A C G A G A T G									
...										
GLY	GLY	SER	PHE	THR	HIS	ASN	THR	ASP	ASP	...
G G C G G G T C A T T A C A C A C A C C G A T G A C...										
2050	2060	2070...	2080	2090	2100	2110	2120	2130	2140	2150
...	SER	LYS	ALA	SER	VAL	VAL	PHE	GLY	THR	LYS
...	A G T A A A G C C T C T G T G T C T T G C A C A A A									
...										
ARG	GIN	GLU	GLU	VAL	LYS	LYS	...	***		
A G A C A A G A A G A A G T T A A G T A G										
2110	2120	2130	2140	2150	2160	2170	2180	2190	2200	2210

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FIG.3A

Restriction map of *M. catarrhalis* strain 3 *tbpB* gene

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NcoI
PaiI
Sau96I
SspI
StyI
TaqI
XbaI

FIG.3B

FIG. 4A

M. catarrhalis strain 3 *tbpB* sequence

FIG.4B

GLN	ASP	VAL	PRO	THR	ASP	LYS	ASN	LYS	LYS	...
C A A G A T G T G C C A A C C G A T A A A A A A A A...										
250	260	270	280	290	300					
...	ASP	GLU	VAL	SER	GLY	ILE	GLN	GLU	PRO	ALA
...	G A T G A A G T G T C A G G C A T T C A A G A A C C T G C C									
...										
MET	GLY	TYR	GLY	VAL	GLU	LEU	LYS	LEU	ARG	...
A T G G G T T A T G G C G T G G A A T T A A A G C T T C G T...										
310	320	330	340	350	360					
...	ASN	TRP	ILE	PRO	GLN	GLU	GLN	GLU	GLU	HIS
...	A A C T G G A T A C C A C A A G A A C A G G A A A C A T									
...										
ALA	LYS	ILE	ASN	THR	ASN	ASP	VAL	VAL	LYS	...
G C C A A A T C A A T A C A A A T G A T G T T G T A A A A...										
370	380	390	400	410	420					
...	LEU	GLU	GLY	ASP	LEU	LYS	HIS	ASN	PRO	PHE
...	C T T G A A G G T G A C T T G A A G C A T A A T C C A T T T									
...										
ASP	ASN	SER	ILE	TRP	GLN	ASN	ILE	LYS	ASN	...
G A C A A C T C T A T T G G C A A A C A T C A A A A T...										
430	440	450	460	470	480					
...	SER	LYS	GLU	VAL	GLN	THR	VAL	TYR	ASN	GLN
...	A G C A A A G A A G T A C A A A C T G T T T A C A A C C A A									
...										

FIG.4C

GLU LYS GIN ASN ILE GLU ASN GLN ILE LYS ...
G A G A G C A A A C A T T G A A A T C A A A T C A A A ...
490 500 510 ...
... LYS GLU ASN LYS GLU LEU ASP LYS THR ALA
... A A A G A A A T A A G A A C T T G A T A A A C G G C A
... 520 530 540

LEU LYS ALA LEU ILE GLU LYS VAL LEU ASP ...
C T A A A G C T C T T A T T G A A A G T T C T T G A T ...
550 560 570 ...
... ASP TYR LEU THR SER LEU ALA LYS PRO ILE
... G A C T A T C T A A C A A G T C T T G C T A A C C C A T T 6/73
... 580 590 600

TYR GLU LYS ASN ILE ASN ASP SER HIS ASP ...
T A T G A A A A A T A T T A A T G A T T C A C A T G A T ...
610 620 630 ...
... LYS GIN ASN LYS ALA ARG THR ARG ASP LEU
... A A G C A G A A T A A A G C A C T C G T G A T T G
... 640 650 660

LYS TYR VAL ARG SER GLY TYR ILE TYR ARG ...
A A G T A T G T G C G T T C T G G T T A T T A T C G C ...
670 680 690 ...
... SER GLY TYR SER ASN ILE ASP ILE GLN LYS
... T C A G G T T A T T C T A A T C G A C A T T C A A A G
... 700 710 720

FIG. 4D

LYS	ILE	ALA	LYS	THR	GLY	PHE	ASP	GLY	ALA	...
A A A A T A G C T A A A A C T G G T T G A T G G T G C T...										
730	740	750...								
	...	LEU	PHE	TYR	LYS	GLY	THR	GLN	THR	ALA
		...	TTA TTT TAA GGT ACACAA							LYS
			760							780
GLN	LEU	PRO	VAL	SER	GLU	VAL	LYS	TYR	LYS	...
C A A T T G C C T G T A T C T G A G G T T A A G T A T A A A...										
790	800	810...								
	...	GLY	THR	TRP	ASP	PHE	MET	THR	ASP	ALA
		...	G G C A C T T G G G A T T T A T G A C C G A T G C C A A A							LYS
			820							17/73
LYS	GLY	GIN	SER	PHE	SER	SER	PHE	GLU	ARG	...
A A A G G A C A A T C A T T A G C A G T T G A A A G A...										
850	860	870...								
	...	ARG	ALA	GLY	ASP	ARG	TYR	SER	ALA	MET
		...	C G A G C T G G T G A T C G C T A T A G T G C A A T G T C T							SER
			880							900
SER	HIS	GLU	TYR	PRO	SER	LEU	LEU	THR	ASP	...
T C C C A T T G A G T A C C C A T C T T A T T A A C T G A T...										
910	920	930...								
	...	ASP	LYS	ASN	LYS	PRO	ASP	ASN	TYR	ASN
		...	G A T A A A A C A A A C C A G A T A A T T A A C G A T							ASP
			940							960

FIG. 4E

GLU	TYR	GLY	HIS	SER	GLU	PHE	THR	VAL	...	
G A A T A T G G T C A T A G C A G T G A G T T A C G G T A...	970	980	990...							
...	ASP	PHE	SER	LYS	SER	LEU	THR	GLY	GLY	
...	G A T T T A G T A A A G C C T A A C A G G T G G G	1000	1010							
									1020	
18/73										
LEU	PHE	SER	ASN	LEU	GLN	ASP	HIS	HIS	LYS	...
C T G T T A G T A A C C T A C A A G A C C A C C A T A A G...	1030	1040	1050...							
...	GLY	LYS	VAL	THR	LYS	THR	LYS	ARG	TYR	ASP
...	G G C A A G G T T A C G A A A A C C A A A C G C T A T G A C	1060	1070							
										1080
1140										
ILE	ASN	ALA	ARG	IIE	His	GLY	ASN	ARG	PHE	...
A T C A A T G C C C G T A T C C A C G G T A A C C G C T T C...	1090	1100	1110...							
...	ARG	GLY	SER	ALA	THR	ALA	IIE	ASN	LYS	ASP
...	C G T G G C A G T G C C A C C G C A A T C A A T A A A G A T	1120	1130							
										1140
1150										
ASN	GLU	SER	LYS	ALA	LYS	HIS	PRO	PHE	THR	...
A A T G A A A G C A A A G C C A A G C C A A C A C C C T T A C C...	1160	1170...								
...	SER	ASP	ALA	ASP	ASN	ARG	LEU	GLU	GLY	GLY
...	A G C G A T G C C G A C A A T A G G C T A G A A G G C G G T	1180	1190							
										1200

FIG. 4F

FIG.4G

ILE	ASP	LEU	THR	GLN	GLY	ASN	ASP	PHE	VAL	...
A T A G A C C C T T A C T C A A G G T A A T G A T T G T A...	1450	1460	1470...							
...	LYS	THR	IIE	ASP	LYS	GLU	LYS	PRO	ALA	THR
...	A A A A C C A T T G A T A A G A A G C C A G C C A C C	1480	1490	1500						
...										
THR	THR	ASN	GLN	ALA	GLY	GLU	PRO	LEU	THR	...
A C T A C C A A T C A A G C A G G C G A G C C T T G A C G...	1510	1520	1530...							
...	VAL	ASN	ASP	LYS	VAL	ARG	VAL	GLN	VAL	CYS
...	G T G A A T G A T A A G G T T C G G G T A C A A G T T T G T	1540	1550	1560	1570	1580...	1590...	1600	1610	1620
...										
CYS	SER	ASN	LEU	GLU	HIS	LEU	LYS	PHE	GLY	...
T G T A G C A A T C T T G A G C A T C T A A A T T T G G C...	1570	1580	1590...							
...	SER	LEU	SER	IIE	GLY	ASP	SER	ASN	SER	VAL
...	T C A C T G A G T A T C G G T G A T A G T A A T A G C G T C	1600	1610	1620						
...										
PHE	LEU	GLN	GLY	GLU	ARG	THR	ALA	THR	LYS	...
T T T T A C A A G G T G A A C G C A C C G C T A C C A A A...	1630	1640	1650...							
...	GLY	ASP	LYS	ASP	LYS	ALA	MET	PRO	VAL	ALA
...	G G T G A T A A G A T A A G C C A T G C C A G T T G C A	1660	1670	1680						
...										

FIG.4H

GLY ASN ALA LYS TYR ARG GLY THR TRP ALA ...
G G A A T G C T A A T A C C G T G G T A C A T G G G C A ...
1690 1700 ...
... GLY TYR VAL ALA GLY SER GLY ASN THR SER
... G G C T A T G T T G C A G G C T C T G G C A A T A C C A G C
1720 1730 1740 21/73

LYS ALA TYR GLU ALA GIN GIN PHE ALA ASP ...
A A A G C C T A T G A A G C C C A A C A A T T T G C T G A C ...
1750 1760 1770 ...
... ASN ALA ASN ARG ALA GLU PHE ASP VAL ASP
... A A T G C C A A C C G T G C C G A G T T G A T G T A G A C
1780 1790 1800

PHE ALA ASN LYS SER LEU THR GLY LYS LEU ...
T T T G C T A A C A A A A G C C T A A C T G G T A A G C T T ...
1810 1820 1830 ...
... ILE PRO ASN THR SER SER ASP GLY LYS SER
... A T T C C A A A T A C G A G C A G T G G T A A A T C T
1840 1850 1860

ALA PHE ASP ILE THR ALA THR ILE ASP GLY ...
G C T T T G A T A C T G C T A C A A T T G A T G G C ...
1870 1880 1890 ...
... ASN GLY PHE SER GLY LYS ALA ASN THR PRO
... A A T G G T T A G T G G T A A A G C C A A T A C A C C A
1900 1910 1920

FIG.4I

ASP ILE GLU THR GLY LEU LYS ILE ASP ...
GATTGAAACAGGTGTTAACAGTAAAGATTTGAC...
1930 1940 1950... 1960 1970 1980

... SER LYS ASN SER GLU SER GLY ARG VAL ILE
... AGTAAAGAACAGTGAAAGCAGCTAACAGTAAAT 22/73

VAL LYS ASP ALA ILE VAL ILE GLY GLY PHE ...
GTGAAAGATGCTATAGTTAGTATAGTAAAGCTT...
1990 2000 2010... 2020 2030 2040

... TYR GLY PRO GIN ALA ASN GLU LEU GLY GLY
... TATGGTCACAAAGCTAAATGAAACTGGTGGC 22/73

SER PHE THR TYR LYS SER ASN ASP ALA GLY ...
TCATTACCTACAAAGAACAGTAAAGCTGGAA...
2050 2060 2070... 2080 2090 2100

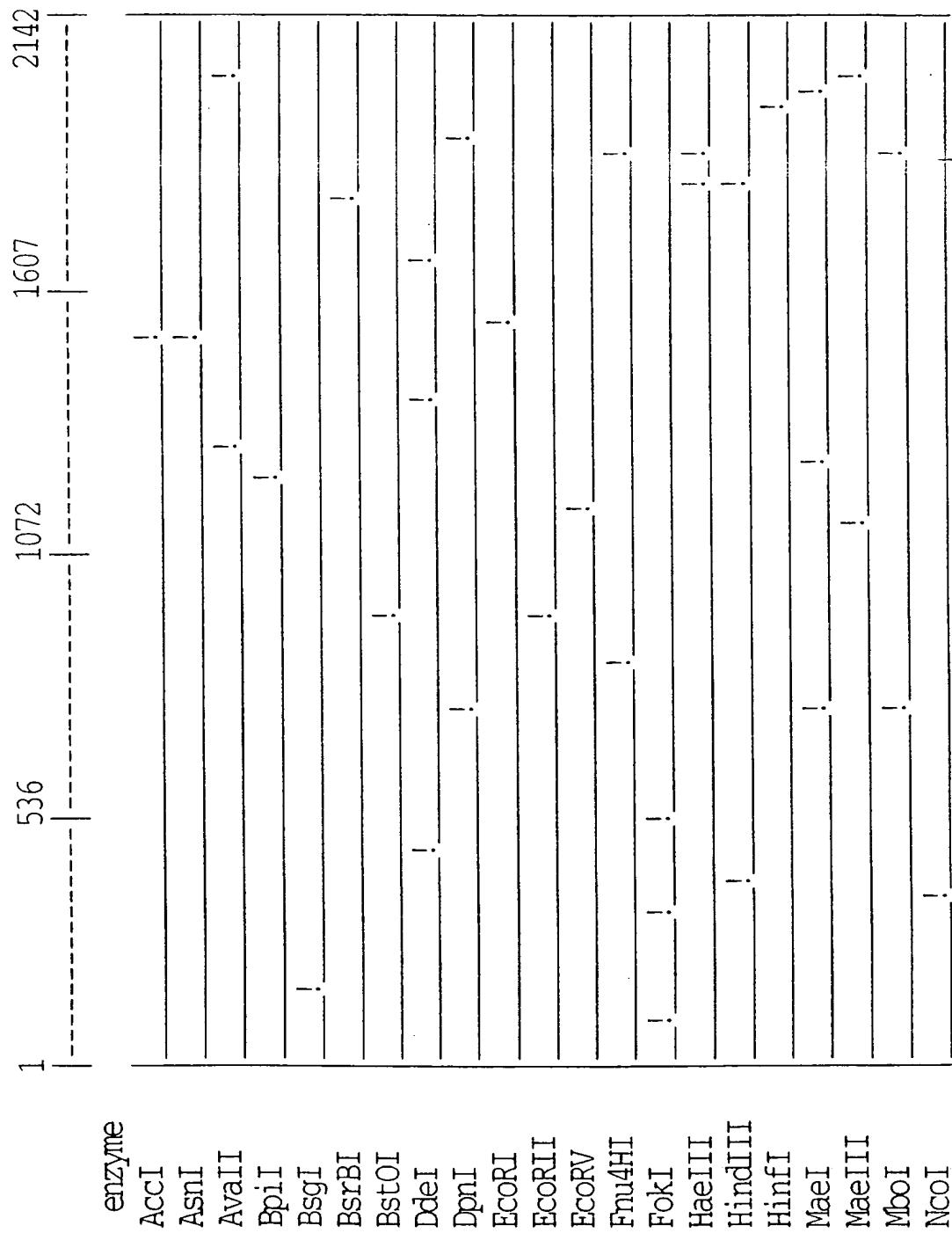
... ASN GLN ASP LYS ASP SER SER ALA SER VAL
... AATCACAAAGAACAAAGACAGTAGTGGTGG 22/73

VAL PHE GLY ALA ARG LYS GLN GLU VAL ...
GTCCTTGGTGCACAAAGAACAAAGTGC...
2110 2120 2130

... LYS PRO ***
... AAAACCAATGA

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FIG.5A

Restriction map of *M. cattarrhalis* strain LES1 *tbpB* gene

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FIG.5B

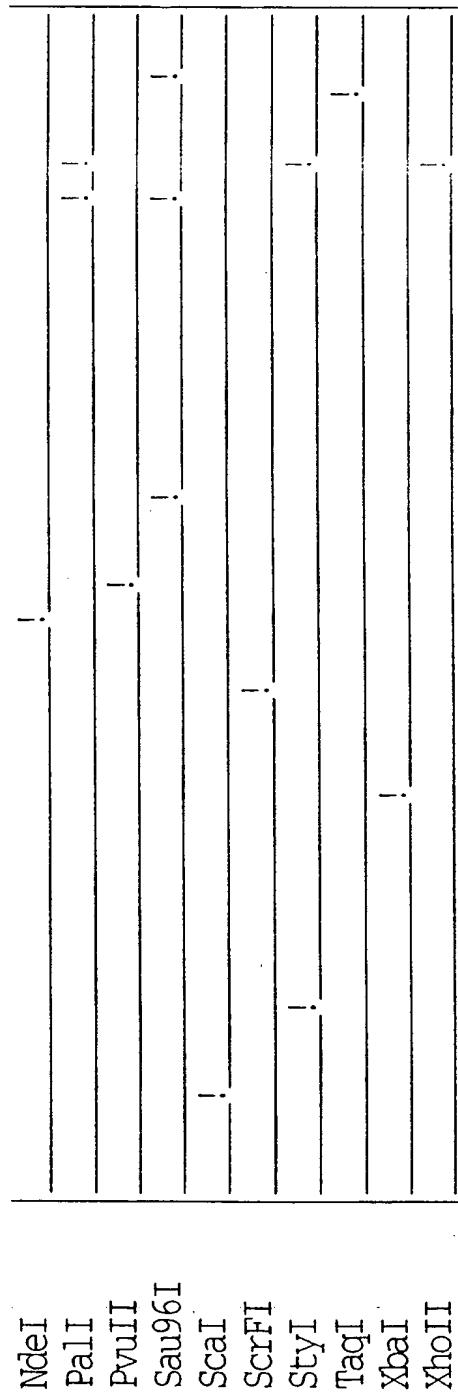


FIG. 6A

M. catarrhalis strain LES1 tbpB sequence

FIG. 6B

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GLY	THR	GLY	SER	ALA	ASN	THR	PRO	GLU	PRO	...
G	G	T	A	C	A	G	G	C	A	...
250	260	270	280	290	300					
...					
GLU	LYS	GLU	GLN	VAL	SER	SER	IIE	GIN	GLU	...
G	A	A	A	G	A	C	A	G	A	...
310	320	330	340	350	360					
...					
LEU	ARG	ASN	ALA	HIS	PRO	LEU	ASN	PRO	ASN	...
C	T	T	C	G	T	A	C	C	T	...
370	380	390	400	410	420					
...					
LEU	ASP	GLN	LYS	ASP	LEU	VAL	ALA	VAL	GLU	...
T	T	A	G	C	A	A	G	T	G	...
430	440	450	460	470	480					
...					

FIG. 6C

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ASN	LEU	ILE	GLU	TYR	LEU	LYS	SER	SER	...
AAT	CTT	ATT	GAA	TAC	CTT	AAA	ATC	ATC	...
490	500	510...	520	530	540				
...	GLU	VAL	VAL	SER	LYS	PHE	GLU	ALA	GLN
...	GAG	GTT	GTT	GTA	GTA	ATTA	GAA	GCA	CAA
...									
GLY	GLY	ILE	GLU	ASN	ASN	THR	ARG	LEU	THR
GCG	GCT	AT	TGA	AA	AA	AC	AC	CTG	ACAA
550	560	570...	580	590	600				
...	HIS	LYS	ASP	LEU	SER	SER	SER	GLU	GLN
...	CAC	AAA	GAT	TAT	CA	TCA	GAG	CAA	AAA
...									
ALA	LYS	VAL	LYS	GLU	ALA	LEU	ASP	ASN	ALA
GCA	AAA	GTC	AAA	GCA	AGC	GGT	GGT	CAA	ATGCTT
610	620	630...	640	650	660				
...	LEU	THR	GLN	PHE	ALA	GLN	GLU	LYS	TYR
...	TTAAC	CTCAA	ATT	TGCCC	AAAGAA	AAATACAA	AGA	AAATACAA	AG
...									
GLU	LEU	ILE	GLU	ASN	ALA	HIS	ASP	LYS	LYS
GAG	CTA	ATT	GAG	AA	ACG	CCC	CATG	ATAAA	...
670	680	690...	700	710	720				
...	SER	ASP	ALA	ARG	ASN	ARG	ASP	LEU	GLU
...	TCTGACG	CCGCAAC	CGTGA	TCTAG	AAATG	ATGAA	TAT		TYR

FIG.6D

VAL	LYS	SER	GLY	PHE	ASN	TYR	LEU	SER	GLY	...
G T C A A G T C T G G T T A A C T A T C T T C T G G A...										
730	740	750...								
...	TYR	THR	ALA	THR	ASP	HIS	ASP	LYS	LYS	THR
...	T A T A C C G C C A C C G A C C G A C A C A A A A C C									
760	770	780								
...										
ASN	TYR	ARG	GLY	TYR	TYR	GLY	ALA	LEU	TYR...	...
A A T T A T C G T G G C T A T T A T G G T G C G T T A T...										
790	800	810...								
...	TYR	LYS	GLY	SER	GLU	THR	ALA	LYS	GLU	LEU
...	T A T A A A G G C A G C G A A A C C G C C A A A G A G C T A									
820	830	840								
...										
PRO	GLN	THR	SER	ALA	LYS	TYR	LYS	GLY	TYR	...
C C A C A A C A A G T G C A A A T A T A A G G T T A T...										
850	860	870...								
...	TRP	ASP	PHE	MET	THR	ASP	ALA	THR	LEU	ASP
...	T G G G A C T T A T G A C A									
...	880	890	900							
...										
ASN	LYS	TYR	THR	ASP	LEU	PRO	GLY	IIE	ALA	...
A A C A A A T A C A C G G A T T T G C C A G G T A T C G C C...										
910	920	930...								
...	ARG	GLN	THR	GLN	TRP	ARG	SER	LEU	VAL	SER
...	A G A C A A A C C C A G T G G C G T A G T C T T G T T T C T									
940	950	960								
...										

FIG.6E

THR ASP GLU TYR ALA THR LEU LEU THR ASP ...
 A C T G A T G A G T A T G C A A C G C T T G A C A G A C ...
 970 990...
 ... LYS ASN ASN LYS PRO SER ASP TYR ASN GLY
 ... A A A A A T A A C A A G C C A G T G A T T A C A A T G G T
 1000 1020 1020
 ...
 ...
 ALA TYR GLY HIS SER GLU PHE ASP VAL ...
 G C A T A T G G T C A T A G C A G T G A A T T G A T G T T ...
 1030 1050...
 ... ASN PHE ALA ASP LYS ILE LYS GLY LYS 29/73
 ... A A T T T G C T G A T A A A A A A A T T A A G G C A A A
 1060 1070 1080
 ...
 ...
 LEU ILE SER ASN GIN LEU SER GLY THR ALA ...
 C T T A T C A G T A A T C A G T T A T C A G G C A C A G C T ...
 1090 1110...
 ... VAL THR ALA LYS GLU ARG TYR LYS ILE GLU
 ... G T A A C C G C C A A A G A G C G T T A T A G A A
 1120 1130 1140
 ...
 ...
 ALA ASP ILE HIS GLY ASN ARG PHE ARG GLY ...
 G C T G A T A T C C A C G G C A A C C G C T T C C G T G G C ...
 1150 1160 1170...
 ... SER ALA THR ALA SER ASP LYS ALA GLU ASP
 ... A G T G C C A C C G C A A G C G A T A A A G C A G A C
 1180 1190 1200

FIG. 6F

SER LYS THR GLN HIS PRO PHE THR SER ASP ...
 A G C A A A A C C C A A C A C C C T T A C C A G C G A T ...
 1210 1230...
 1220 ...
 ... ALA THR ASN LYS LEU GLU GLY GLY PHE TYR
 ... G C T A C A A A C A A G C T A G A A G G T G G T T T A T
 1240 1250 1260
 ...
 ...
 GLY PRO LYS GLY GLU GLU LEU ALA GLY LYS ...
 G G A C C A A A A G G C G A G G C T G G C A G G T A A A ...
 1270 1290...
 1280 ...
 ... PHE LEU THR ASP ASN LYS LEU PHE GLY
 ... T T C T T A A C C G A T G A C A A C A A C T C T G G G
 1300 1310 1320
 ...
 ...
 VAL PHE GLY ALA LYS ARG ASP LYS VAL GLU ...
 G T C T T T G G T G C T A A A C G A G A T A A A G T A G A A ...
 1330 1350...
 1340 ...
 ... LYS THR GLU ALA ILE ILE ASP ALA TYR ALA
 ... A A A A C C G A A G C C A T C T T A G A T G C C T A T G C A
 1360 1370 1380
 ...
 ...
 LEU GLY THR PHE ASN ASN THR ASN LYS ALA ...
 C T T G G G A C A T T A A T A C A A A T A A G C A ...
 1390 1410...
 1400 ...
 ... THR THR PHE THR PRO PHE THR LYS LYS GLN
 ... A C C A C A T T C A C C C A T T A C C A A A A C A A
 1420 1430 1440

FIG. 6G

FIG. 6H

FIG. 61

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ASN GLY TRP THR GLY LYS ALA SER THR THR ...
AAT GGC TGG CAA GGC AAA GCC AGC CAC C...
1930 1940 1950... 1960 1970 1980 1990 2000 2010... 2020 2030 2040 2050 2060 2070... 2080 2090 2100 2110 2120 2130... 2140 ...
SER SER SER THR GLY SER ILE VAL ILE ...
TCT AGC CAG TAG CAA GGC AAA TCC ATCGT CATT C...
1990 2000 2010... 2020 2030 2040 2050 2060 2070... 2080 2090 2100 2110 2120 2130... 2140 ...
GLY PRO ASN ALA ASN GLU MET GLY GLY SER ...
GGT CCA AAATGCA AAC GAG ATGGCGT CAA...
2050 2060 2070... 2080 2090 2100 2110 2120 2130... 2140 ...
SER VAL VAL PHE GLY THR LYS ARG GLN GLN ...
TCT GTGGT CTT GGC AAC AAA AGAACAA CAA...
2110 2120 2130... 2140 ...

FIG.7A Alignment of *M. catarrhalis* TbpB protein sequences

FIG. 7B

LSSLLENKIFHSNDGTTKATTTRDLKYDGYYLANDGMLTVKTD-KLMNLGPVGGVFY
 ... IKA.T ... K ... V ... A ... NP ... S ...
 ... K ... V ... Q ... KS ... E ... FNLSGYTATDHDK --- TNVR YY ALY.
 QEKYKEL ENVAH KKSD RN E ... KS ... FNLSGYTATDHDK --- TNVR YY ALY.
 KPIY KN NY H KQN R ... RS ... IYRSGYSNIIIP. --- IAKT FD AL ...
 KPIY KN ND H KQN R ... RS ... IYRSGYSNIDIQK --- IAKT FD AL ...
 210 220 230 240 250
 260 270 280 290 300
 NGTTTAKELPTQDAVKYKGHMDFMIDVANRNRSEVAKNSQA
 ... S ... KK ... TY ...
 ... KQ ... L ...
 K. SE ... QTS. - Y ... ATLDWKYTDLPGIAR. T
 Q. Q. Q. VSQ- T ... AKKGQSF. FGTSQRL.
 K. Q. Q. VSE- T ... AKKGQSF. FERRAGDR
 310 320 330 340 350
 GMYGASSKDEYNRLLTEDSAPDHSGEYGHISSEFTVNFKEKKLTKLFSNQDRH
 ... W. ... A.A. ... NY ... E ... S.
 ... R. ... D. KNK. ERYN ... D ... E ... SR
 Q.-RSLV T ... AT ... DRNNK. SDYN A ... D ... AD ... IK ... I ... QLSG-
 ... DR. S.M. YH. PS ... D. KNK. NYN ... D. SK. S.K.E.S. I. G.
 -- SAM. H- PS ... DRNNK. NYND ... D. SK. S ... G ... H.
 360 370 380 390 400
 KGNVTKTERYDIDANIHKGRFGSATASNKNDTSK--HPFTSDAN
 ... QK ... K ... K.D ... D.AED ... SK ...
 ... K ... K ... Y ... D.AEA ... TK ...
 -TA ... AK ... K.E.D ... D.AED ... TQ ... T
 ... S.N. K ... Y ... DTEA ... SK ...
 ... K ... K ... N.R ... I ... DNE ... AK ... D
 4223
 R1
 MB5
 LES1
 Q8
 3

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FIG. 7C

410	420	430	440	450
NRLEGGFYGPKGEELAGKFLTDNKLFGVFGAKRESKAAEKTTEAILDAYALGIFTNTSN				
DK.....	D.....	Q.GWV.....		KPG.....
S.....	MA.....		G.....	KNN.....
K.....		D.....	D- V.....	NT.....
S.....	NA.....		E.K.....	KPG.....
		D.....	Q. E.K. -	KSG.....
				170
				160

DKPESATNEAGETIMVNDEVSKTKYG--KNFEYLKFGELSIGGSHSVELLOGERTATTIG
 E..K.....K.....V.....
 N..D.....K.....YGR.....V.T.N.....
 ...T.....K.....I.....V.D.....
 E..K.....K.....I.....YGR.....
 S.....D.....V.D.....S.....D.....N.....K.

4223
R1
MB5
LES1
Q8
3
360 570 580 590 600
E--KAVPTITGTAKYLGWGYITGKDGTG--GKSFTDAQDVADEDI
.....K.....A.SSK.STD.G...K.I.....
.....K.....S-----S...NE.....
.....K.....A...--...NE...I.....
...E.....S...--...NE...I...V
DD M VA N B T A VA SGNTSKAYEAOQ A NANR E V

FIG. 7D

610 DFGNKVSSGKLITKGRQDFV--FSITGQIAGNGMTGTASTTIKADAGGYKIDSSTGKS
 ..EK...N...T...D....--N...E.....K...AE...N.....
 ..EK...K...T...D....--N...D.....K.....
 ..ER...K...T...Q...T....--N...K...E.....K.....
 ..ER...K...T...Q...--N.....A...NW.....
 ..A...LT...PNTSS...GKSA...D...AT...D...FS...K...N...PDIET...L...K...N...SE...SG
 620 630 640 650
 660 670 680
 690 700
 -IVIKDANVTGFEYGPNANEMGGSFTHNA-----DDSKASWWFGTKQQEVK-*
 -...V.....T.....S-----CN.G.V.....K...-...K*
 -...E.....T-----T-----E...-*
 -...EN.E.....DT-----*
 -...EN.K.....DT-----E...-*
 RVTV...I.I.....Q...L.....YKSNDAGNQDK...S.....ARK.....P*
 37/73
 R1
 M35
 LES1
 Q8
 3

FIG. 8A

M. catarrhalis strain 4223 *tboA* - *orf3* - *tboB* locus gene sequences

FIG.8B

VAL	VAL	THR	ALA	LYS	ASN	ALA	ARG	LYS	...	
G T T G T A A C A G C G A A G A A A A C G C C C G C T A A A...										
250	260	270...								
...	ALA	ASN	GLU	VAL	THR	GLY	LEU	GLY	LYS	
...	G C C A A C G A A G T T A C A G G C T T G G T A A G G T G									
280	290	300								
...								
VAL	LYS	THR	ALA	GLU	THR	ILE	ASN	LYS	GLU	...
G T C A A A A C T G C C G A G A C C A T C A A T A A A G A A...										
310	320	330...								
...	GLN	VAL	LEU	ASN	ILE	ARG	ASP	LEU	THR	ARG
...	C A A G T G C T A A A C A T T C G A G A C T T A A C A C G C									
340	350	360								
...								
TYR	ASP	PRO	GLY	ILE	ALA	VAL	VAL	GLU	GIN	...
T A T G A C C C T G G C A T T G C T G C T G T G G T T G A G C A A...										
370	380	390...								
...	GLY	ARG	GLY	ALA	SER	SER	GLY	TYR	SER	ILE
...	G G T C G T G G G C A A G C T C A G G C T A T T C T A T T									
400	410	420								
...								
ARG	GLY	MET	ASP	LYS	ASN	ARG	VAL	ALA	VAL	...
C G T G G T A T G G A T A A A A T C G T G T G G C G G T A A...										
430	440	450...								
...	LEU	VAL	ASP	GLY	ILE	ASN	GLN	ALA	GLN	HIS
...	T T G G T T G A T G G C A T C A A T C A A G C C C A G C A C									
460	470	480								
...								

FIG. 8C

TYR	ALA	LEU	GLN	GLY	PRO	VAL	ALA	GLY	LYS	...												
1	A	T	G	C	C	T	A	C	A	G	G	C	C	T	G	T	G	G	C	A	...	
490	500	510...	520	530	540	550	560	570...	580	590	600	610	620	630...	640	650	660	670	680	690...	700	710
ILE	GLU	TYR	GLU	ASN	VAL	ARG	SER	VAL	GLU	...												
A	T	A	G	A	A	T	C	C	G	T	T	G	A	G	
550	560	570...	580	590	600	610	620	630...	640	650	660	670	680	690...	700	710	720	730	740	750	760	
GLY	SER	GLY	ALA	LEU	SER	GLY	SER	VAL	ALA	...												
G	G	C	T	G	G	C	A	T	T	A	T	C	T	G	G	C	A	
610	620	630...	640	650	660	670	680	690...	700	710	720	730	740	750	760	770	780	790	800	810	820	
LYS	ASP	GLY	LYS	ASP	TRP	GLY	VAL	GLN	THR	...												
A	A	A	G	A	T	A	A	G	A	C	C	
670	680	690...	700	710	720	730	740	750	760	770	780	790	800	810	820	830	840	850	860	870	880	

FIG.8D

TRP VAL ASN SER VAL ALA ALA GLY LYS ...
 T G G G T T A A T T C T G T G C A G C A G C A G C A A G ...
 730 740 750 ...
 ... ALA GLY SER PHE SER GLY LEU ILE TYR
 ... G C A G G T T C T T A G C G G T C T T A T C A T C T A C
 760 770 780 ...
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THR ASP ARG ARG GLY GLN GLU TYR LYS ALA ...
 A C C G A C C G C C G T G G T C A A G A A T A C A A G G C A ...
 790 800 810 ...
 ... HIS ASP ASP ALA TYR GLN GLY SER GLN SER
 ... C A T G A T G A T G C C T A T C A G G T A G C C C A A A G T
 820 830 840 ...
 ...

PHE ASP ARG ALA VAL ALA THR THR ASP PRO ...
 T T T G A T A G A G C G T G G C A A C C A C T G A C C C A ...
 850 860 870 ...
 ... ASN ASN ARG THR PHE LEU ILE ALA ASN GLU
 ... A A T A A C C G A A C A T T T A A T A G C A A A T G A A
 880 890 900 ...
 ...

CYS ALA ASN GLY ASN TYR GLU ALA CYS ALA ...
 T G T G C C A A T G G T A A T T A T G A G G C G T G C T ...
 910 920 930 ...
 ... ALA GLY GLY GIN THR LYS LEU GLN ALA LYS
 ... G C T G G C G G T C A A A C C A A C T T C A A G C C A A G
 940 950 960 ...
 ...

FIG.8E

PRO THR ASN VAL ARG ASP LYS VAL ASN VAL ...
 C C A A C C A A T G T G C G T G A T A A G G T C A A T G T C ...
 970 980 ...
 ... LYS ASP THR GLY PRO ASN ARG LEU ILE
 ... A A A G A T T A T A C A G G T C C T A A C C G C C T T A T C
 1000 1020 ...

 PRO ASN PRO LEU THR GLN ASP SER LYS SER ...
 C C A A C C A C T C A C C C A A G A C A G C A A T C C ...
 1030 1040 ...
 ... LEU LEU LEU ARG PRO GLY TYR GLN LEU ASN
 ... T T A C T G C T T C G C C A G G T T A T C A G C T A A A C
 1060 1070 ...

 ASP LYS HIS TYR VAL GLY GLY VAL TYR GLU ...
 G A T A A G C A C T A T G T C G G T G G T G T A T G A A ...
 1090 1100 ...
 ... ILE THR LYS GLN ASN TYR ALA MET GLN ASP
 ... A T C A C C A A A C A A A C T A C G C C A T G C A A G A T
 1120 1130 ...

 LYS THR VAL PRO ALA TYR LEU ALA VAL HIS ...
 A A A C C G T G C C T G C T T A T C T G G G T T C A T ...
 1150 1160 ...
 ... ASP ILE GLU LYS SER ARG LEU SER ASN HIS
 ... G A C A T T G A A A A T C A A G G C T C A G C A A C C A T
 1180 1200 ...

FIG.8F

ALA GLN ALA ASN GLY TYR TYR GLN GLY ASN ...
 G C C A A G C C A A T G G C T A T T A T C A A G G C A A T ...
 1210 1220 1230 ...
 ... ASN LEU GLY GLU ARG ILE ARG ASP THR ILE
 ... A A T C T T G G T G A A C G C A T T C G T G A T A C C A T T
 1240 1250 1260
 ...

 GLY PRO ASP SER GLY TYR GLY ILE ASN TYR ...
 G G G C C A A G A T T C A G G T T A T G G C A T C A A C T A T ...
 1270 1280 1290 ...
 ... ALA HIS GLY VAL PHE TYR ASP GLU LYS HIS
 ... G C T C A T G G C G T A T T T A T G A T G A A A C A C 43/73
 ...
 1300 1310 1320
 ...

 GLN LYS ASP ARG LEU GLY LEU GLU TYR VAL ...
 C A A A A G A C C G C C T A G G C T T G A A T A T G T T ...
 1330 1340 1350 ...
 ... TYR ASP SER LYS GLY GLU ASN LYS TRP PHE
 ... T A T G A C A G C A A A G G T G A A A T G G T T
 ...
 1360 1370 1380
 ...

 ASP ASP VAL ARG VAL SER TYR ASP LYS GLN ...
 G A T G A T G T G C G T G T G T C T T A T G A T A G C A A ...
 1390 1400 1410 ...
 ... ASP ILE THR LEU ARG SER GLN ILEU THR ASN
 ... G A C A T T A C G C T A C G C A G C C A G C T G A C C A A C
 1420 1430 1440
 ...

FIG.8G

THR HIS CYS SER THR TYR PRO HIS ILE ASP ...
 A C G C A C T G T T C A A C C T A T C C G C A C A T T G A C ...
 1450 1460 1470 ...
 ... LYS ASN CYS THR PRO ASP VAL ASN LYS PRO
 ... A A A A T T G T A C G C C T G A T G T C A A T A A C C T
 1480 1490 1500
 ...
 44/73

PHE SER VAL LYS GLU VAL ASP ASN ASN ALA ...
 T T T C G G T A A A G A G G A T A C A A T G C C ...
 1510 1520 1530 ...
 ... TYR LYS GLU GLN HIS ASN LEU ILE LYS ALA
 ... T A C A A A G A A C A G C A C A T T A A T C A A A G C C
 1540 1550 1560
 ...

VAL PHE ASN LYS LYS MET ALA LEU GLY SER ...
 G T C T T A A C A A A A A T G G C T T G G C A G T ...
 1570 1580 1590 ...
 ... THR HIS HIS ILE ASN LEU GLN VAL GLY
 ... A C G C A T C A C A T C A A C C T G C A A G T T G G C
 1600 1610 1620
 ...

TYR ASP LYS PHE ASN SER SER LEU SER ARG ...
 T A T G A T A A T T C A A T T C A A G C C T G A G C C G T ...
 1630 1640 1650 ...
 ... VAL GLU TYR ARG LEU ALA THR HIS GLN SER
 ... G T A G A A T A T C G T T G G C A A C C A T C A G T C T
 1660 1670 1680
 ...

FIG.8H

TYR	GLN	LYS	LEU	ASP	TYR	THR	PRO	PRO	SER	...
T A T C A A A A C T T G A T T A C A C C C A C C A A G T...										
1690										1710...
	...	ASN	PRO	ILE	PRO	ASP	LYS	PHE	LYS	PRO
		ILE
		1740
ILE	GLY	SER	ASN	ASN	LYS	PRO	ILE	CYS	LEU	...
T T A G G T T C A A A C A A C A A A C C C A T T T G C C C T T...										
1750										1770...
		1760								
			...	ASP	ALA	TYR	GLY	TYR	GLY	HIS
				ASP
					HIS
						PRO
							
GLN	ALA	CYS	ASN	ALA	LYS	ASN	SER	THR	TYR	...
C A G G C T T G T A A C G C C A A A A C A G C A C T T A T...										
1810										1830...
						
							
								
										1860
GLN	TYR	ASN	GLN	LYS	THR	ASN	THR	ASP	LYS	...
C A A T A C A A C C A A A A A C C A A T A C C G A T A A G...										
1870										1890...
						
							
								
										1910

FIG.8I

ASP LYS GIN ASN PRO ASN SER THR LEU LYS ...
 G A T A A C A A A C C C A A C A C G C A C C C T A A A A ...
 1940 ... 1950 ...
 ... PRO PHE GLU LYS ILE LYS GLN SER LEU GLY
 ... C C C T T G A G A A A T C A A A C A A A G T T T G G G G
 ... 1960 1970 1980 46/73

GLN GLU LYS TYR ASN LYS ILE ASP GLU LEU ...
 C A A G A A A A A T A C A A C A A G A T A G A C G A A C T T ...
 1990 2000 2010 ...
 ... GLY PHE LYS ALA TYR LYS ASP LEU ARG ASN
 ... G G C T T A A A G C T T A T A A A G A T T A C G C A A C
 ... 2020 2030 2040 2050 ...

GLU TRP ALA GLY TRP THR ASN ASP ASN SER ...
 G A A T G G C G G T T G G A C T A A T G A C A A C A G C ...
 2060 2070 ...
 ... GLN ASN ALA ASN LYS GLY THR ASP ASN
 ... C A A C A A A A T G C C A A T A A A G G C A C G G A T A T
 ... 2080 2090 2100 46/73

ILE TYR GIN PRO ASN GIN ALA THR VAL VAL ...
 A T C T A T C A G C C A A A T C A A G C A A C T G T G G T C ...
 2110 2120 2130 ...
 ... LYS ASP ASP LYS CYS LYS TYR SER GLU THR
 ... A A A G A T G A C A A A T G T A A A T A T A G C G A G A C C
 ... 2140 2150 2160

FIG. 8

FIG.8K

GLN GLY PHE ARG MET PRO SER PHE SER GLU ...
C A A G G C T T C G C A T G C C A A G T T C T G A A ...
2410 2420 2430 ...
... MET TYR GLY GLU ARG PHE GLY VAL THR ILE
... A T G T A T G G C G A A C G C T T G G C G T A A C C A T C
2440 2450 2460 ...
48/73

GLY LYS GLY THR GLN HIS GLY CYS LYS GLY ...
G G T A A A G G C A C G C A A C A T G G C T G T A A G G G T ...
2470 2480 2490 ...
... LEU TYR TYR ILE CYS GLN GLN THR VAL HIS
... C T T T A T T A C A T T G T C A G C A G C T G T C C A T
2500 2510 2520 ...
GLN THR LYS LEU LYS PRO GLU LYS SER PHE ...
C A A C C A A G C T A A A C C T G A A A A T C C T T T ...
2530 2540 2550 ...
... ASN GLN GLU ILE GLY ALA THR LEU HIS ASN
... A A C C A A G A A T C G G A G C G A C T T A C A T A A C
2560 2570 2580 ...
HIS LEU GLY SER LEU GLU VAL SER TYR PHE ...
C A C T T A G G C A G T C T G A G G T T A G T T A T T T ...
2590 2600 2610 ...
... LYS ASN ARG TYR THR ASP LEU ILE VAL GLY
... A A A A A T C G C T A T A C C G A T T G A T T G T T G G T
2620 2630 2640 ...

FIG.8L

LYS	SER	GLU	GLU	ILE	ARG	THR	LEU	THR	GLN	...
A A A A G T G A A G A G A T T A G A A C C C T A A C C C A A...										
2650										
...	GLY	ASP	ASN	ALA	GLY	LYS	GLN	ARG	GLY	LYS
	GGT G A T A T G C A G G C A A A C A G C G T G G T A A A									
	2680									
	...									
GLY	ASP	LEU	GLY	PHE	HIS	ASN	GLY	GLN	ASP	...
G G T G A T T G G C T T C A T A A T G G A C A A G A T...										
2710										
...	ALA	ASP	LEU	THR	GLY	ILE	ASN	IIE	LEU	GLY
	G C T G A T T T G A C A G G A A T T A A C A T T C T T G G C									
	2740									
	...									
ARG	LEU	ASP	LEU	ASN	ALA	ASN	SER	ARG	...	
A G A C T T G A C C T A A A C G C T G C C A A T A G T C G C...										
2770										
...	LEU	PRO	TYR	GLY	LEU	TYR	SER	THR	LEU	ALA
	C T T C C C T A T G G A T T A T A C T C A A C A C T G G C T									
	2800									
	...									
TYR	ASN	LYS	VAL	ASP	VAL	LYS	GLY	LYS	THR	...
T A T A A C A A G T T G A T G T T A A A G G A A A A C C...										
2830										
...	LEU	ASN	PRO	THR	LEU	ALA	GLY	THR	ASN	ILE
	T T A A C C C A A C T T G G C A G G A A C A A A C A T A									
	2860									
	...									

FIG.8M

LEU PHE ASP ALA ILE GLN PRO SER ARG TYR ...
 C T G T T G A T G C C A T C C A G C C A T C T C G T T A T ...
 2890 ...
 ... VAL VAL GLY LEU GLY TYR ASP ALA PRO SER
 ... G T G G T G G G C T T G G C T A T G A T G C C C A A G C
 2920 ...
 ...
 2940

GLN LYS TRP GLY ALA ASN ALA ILE PHE THR ...
 C A A A A T G G G A G C A A A C G C C A T A T T A C C ...
 2950 ...
 ... 2970 ...
 ... HIS SER ASP ALA LYS ASN PRO SER GLU LEU
 ... C A T T C T G A T G C C A A A A T C C A A G C G A G C T T
 2980 ...
 ...
 3000 /73

LEU ALA ASP LYS ASN LEU GLY ASN GLY ASN ...
 T T G G C A G A T A A G A C T T A G G T A A T G G C A A C ...
 3010 ...
 ... 3030 ...
 ... ILE GLN THR LYS GLN ALA THR LYS ALA LYS
 ... A T T C A A A C A A A C A A G C C A C C A A G C A A A
 3040 ...
 ...
 3060

SER THR PRO TRP GLN THR LEU ASP LEU SER ...
 T C C A C G C C G T G G C A A C A C T T G A T T G T C A ...
 3070 ...
 ... 3090 ...
 ... GLY TYR VAL ASN ILE LYS ASP ASN PHE THR
 ... G G T T A T G T A A A C A T A A A G A T T T A C C
 3100 ...
 ...
 3120

FIG.8N

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LEU ARG ALA GLY VAL TYR ASN VAL PHE ASN ...
T T G C G T G C T G G C G T A C A A T G T A T T A A T ...
3130 3140 3150 ...
... THR TYR THR THR TRP GLU ALA LEU ARG
... ACC T A T T A C A C C A C T T G G C A G G C T T A C G C
3160 3170 3180 ...
51/73

GLN THR ALA LYS GLY ALA VAL ASN GLN HIS ...
C A A C A G C A A A G G G G C G G T C A A T C A G C A T ...
3190 3200 3210 ...
... THR GLY LEU SER GLN ASP LYS HIS TYR GLY
... A C A G G A C T G A G C C A A G A T A A G C A T T A T G G T
3220 3230 3240 ...
51/73

ARG TYR ALA ALA PRO GLY ARG ASN TYR GLN ...
C G C T A T G C C G C T C C T G G A C G C A A T T A C C A A ...
3250 3260 3270 ...
... LEU ALA LEU GLU MET LYS PHE ***
... T T G G C A C T T G A A A T G A A G T T T A A C C A G T G
3280 3290 3300 ...
51/73

G C T T G A T G T G A T T G G C A T G C C A A T C C ...
3310 3320 3330 ...
... C A A T C A A C C A A T G A A T A A A G C C C C A T T A C
3340 3350 3360 ...
51/73

FIG. 80

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C A T G A G G G C T T A T T C A T C G C T G A G T...
3370
... 3380...
... A T G C T C T C T A G C G G T C A T C A C T C A G A T
3410
3420
...
C A T T A A T T A G C G A T T A T T A T A G T...
3430
3440...
...
... A A T C A C C G C T G C T C T G A T T G A T T A A G T G
3450...
3460
...
... A T G G G T A T T C A A G A A C G A T G T C A T A C T C A G A...
3490
3500...
3510...
... C A C C G T T T A T A G G C T T C T A C T C A A A G A
3520
...
...
C A G G C T T G C C T A A A A A G T C A T C A A C T T C T A...
3550
3560...
... T A T C G C C G A C T T G A T A G C C A C G C A G C A A
3570...
3580...
...
... G C A T T T G A A T G G C T T T G A C G A T T T G G G...
3610
3620...
... C A A A G T T G C T G C G C C A T A A G Q T T G T G C T T
3640
3650...
...
3660

FIG.8P

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T A A T A C G G T C G T T A G C A A A C T G C G G T G G T A G...
3670 3680...
... A G A T A C C A A C G G C A G G C A A C A A A C A G C A G
3690 3700...
C A C T T A G T A C G C C A G C C A A C A G T T A T T G G...
3730 3740...
... T T A A A T T T C A T A G T A G T T C C T A A T T A T
3750 3760...
T A T C A T T G T A A T T C A T G T T A T C G T T A T A...
3790 3800...
... A C A A A T C G T T A T A A T A A C T G T G T C G T G A T A
3810 3820...
A C C A T T A A T C A C A A G T G G G T T A A T G C C T T...
3850 3860...
... T T G C C C A A T G G C A A A T A G G C A C A A T G C T C T
3870 3880...
G C T T G T T C T A T G A T G G T C T A T G A T C A T...
3910 3920...
... C A T T T A T T G A C C T A T T T T T A A T C G T A A
3940 3950...
...
3960

FIG.8Q

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T G T T G T T G A T G T T A G T A A A T T T A T C...
3970
3980
3990...

... A A T C A A C A A T C A C A A A T T A T C A T
4000
4010
4020

...

A G A C G G T A A A C A G G C T C A T T T A C G C A...
4030
4040
4050...

... T A T T T C C C C A G A T G T C T G T A G T T C A T A
4060
4070
4080

...

G A T G A T T T G T A A A C A A A T T G T C G G T C A T T A...
4090
4100
4110...

... T T A T C A A T T G T A A A C T G A T G G C T A A T T T G T
4120
4130
4140

...

A A C C T T A T G G C T A A T G A T A A T G A A T A A A...
4150
4160
4170...

... G C G T T A T A C T G T A T C A A A G A A T G A G T A A A
4180
4190
4200

...

A C C A T C A A T G G T A T C T T A T T A T C A G G...
4210
4220
4230...

... T T G T G T T A A G A T G C C A A T T A G C G A C T
4240
4250
4260

...

FIG.8R

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AA T T G T A A T T A A T T C A T T C A T ...
4280...
... A T T T G T A T T T A A T A C C A T A A A A T G G
4310
4320
...
orf3
MET LEU ALA PHE LEU ILE GLY ALA ...
T A A A T A T G C T C G C T T T G A T A G G A G C T ...
4330
...
... VAL MET THR ILE THR PRO VAL THR THR THR
... G T C A T G A C A A T C A C G C T G T T A T C C A C A 5/73
4360
4370
...
PHE THR PRO THR LYS THR PRO ILE LYS PHE ...
T T C A C C C C A C C A A A A C A C C A T A A A T T T ...
4390
...
... PHE MET ALA GLY LEU THR PHE LEU ILE ALA
... T T T A T G G C T G G C T T G A C T T C T A A T C G C T
4410...
4420
...
...
HIS ILE SER HIS ALA ASP ASP GLY ARG THR ...
C A T A T C A G C C A T G C C G A T G A T G G T C G C A C C ...
4450
...
... ASP ASN GIN GLU LEU ILE ASN GIN GLU ILE
... G A C A A T C A A A G A G C T A A T C A A T C A A T C A A T A
4460
4470...
4480
4490
...
4500

FIG.8S

ALA THR LEU GLU PRO ILE ILE ASN HIS ALA ...
G C C A C C C T T G A A C C C A T C A T T A A C C A T G C T ...
4510 ... 4520 ... 4530 ... 4540 ... 4550 ... 4560

THR PRO LYS ILE GLU PRO ILE LEU ALA GLN ...
A C A C C A A A A T A G A A C C A A T A C T G G C A C A A ...
4570 ... 4580 ... 4590 ... 4600 ... 4610 ... 4620 ... 4630

ALA ASP GLU ALA LEU LEU ASP ASN PRO ...
G C C G A T G A G G C G T T A C T G C T T G A T A A C C C T ...
4640 ... 4650 ... 4660 ... 4670 ... 4680

VAL MET THR ASN HIS MET ALA GLY VAL HIS ...
G T C A T G A C C A A T C A T A T G G C A G G C G T T C A C ...
4690 ... 4700 ... 4710 ... 4720 ... 4730 ... 4740

56/73

FIG.8T

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LYS	ASP	HIS	GLN	ASN	GLY	IIE	LEU	LEU	GLY	...
A A A G A C C A T C A A A A T G G C A T T A C T T G G G	4750	4760	4770	4780	4790	4800				
...	TYR	ALA	ASN	ALA	LEU	ALA	ALA	LEU	ASP	LYS
...	T A T G C C A A T G C C T T G G C T G C T T G G A T A A G									
...										
GLY	ASN	ALA	LYS	ALA	IIE	ASP	GLU	LEU	...	
G G C A A C G C C A A A A A G C C A T T G A G C T A	4810	4820	4830	4840	4850	4860	4870	4880	4890	57/73
...	ARG	ARG	IIE	ILE	ALA	IIE	MET	PRO	GLU	TYR
...	C G T C G C A T C A T C G C C A T C A T G C C T G A A T A T									
...										
ASN	VAL	VAL	ARG	PHE	HIS	LEU	ALA	ARG	ALA	...
A A T G T G G T G C G T T T C A T C T G G C A A G G G C A	4870	4880	4890	4900	4910	4920	4930	4940	4950	4960
...	LEU	PHE	MET	ASP	LYS	GIN	ASN	GLU	ALA	ALA
...	T T A T T A T G G A C A A A C A A A T G A A G C C G C C									
...										
LEU	ASP	GLN	PHE	ASN	LYS	LEU	HIS	ALA	ASP	...
C T T G A C C A G T T A T A A T T A C A T G C T G A C	4930	4940	4950	4960	4970	4980	4990	5000	5010	5020
...	ASN	LEU	PRO	GLU	VAL	ARG	GLN	VAL	VAL	...
...	A A C T T G C C A G A G G T G C G G C A G G T T G T T									
...										

FIG.8U

GLY GLN TYR ARG GLN ALA LEU LYS GLN ARG ...
G G G C A G T A C A G A C A G C A A G C G C T A A A C A A C G A ...
5000...
4990

... ASP SER TRP THR TRP GIN VAL GLY MET ASN
... G A T T C A T G G A C A T G G C A A G T A G G C A T G A A T
5030
5040

...
LEU ALA LYS GLU ASP ASN ILE ASN GLN THR ...
C T G G C C A A G A A G A C A A C A T C A A T C A A A C C ...
5050
5060

... PRO LYS ASN THR THR GIN GLY GLN TRP THR
... C C C A A A A A C A C C A C G C A A G G T C A A T G G A C T
5070...
5080

...
PHE ASP LYS PRO ILE ASP ALA ILE THR LEU ...
T T T G A C A A C C C A T T G A C G C C A T C A C C T A ...
5110
5120

... SER TYR GIN LEU GLY ALA ASP LYS LYS TRP
... A G C T A C C A A T T G G G G G G A T A A A A A G T G G
5130...
5140

...
SER LEU PRO LYS GLY ALA TYR VAL GLY ALA ...
T C T T T G C C C A A A G G G G C A T A T G T G G G A G C G ...
5170
5180

... ASN ALA GIN ILE TYR GLY LYS HIS HIS GLN
... A A C G C C C A A A T C T A T G G C A A A C A T C A A
5200
5220

...
88/73

FIG. 8V

ASN HIS LYS LYS TYR ASN ASP HIS TRP GLY ...
 ATT C A C A A A A A T A C A A C G A C C A T T G G G G C ...
 5230 5240 5250 ...
 ... ARG LEU GLY ALA ASN LEU GLY PHE ALA ASP
 ... AGA C T G G G G C A A A T T T G G G C T T G C T G A T
 5270 5280 5290 ...
 ...
 ALA LYS LYS ASP LEU SER ILE GLU THR TYR ...
 G C C A A A A A G A C C T T A G C A T T G A G A C C T A T ...
 5290 5300 5310 ...
 ... GLY GLU LYS ARG PHE TYR GLY HIS GLU ARG
 ... G G T G A A A A A G A T T T A T G G G C A T G A G C G T
 5330 5340 5350 ...
 ...
 TYR THR ASP THR ILE GLY ILE ARG MET SER ...
 T A T A C C G A C A C C A T T G G C A T A C G C A T G T C G ...
 5350 5360 5370 ...
 ... VAL ASP TYR ARG ILE ASN PRO IYS PHE GIN
 ... G T T G A T T A G A A T C A A C C A A A T T T C A A
 5380 5390 5400 ...
 ...
 SER LEU ASN ALA ILE ASP ILE SER ARG LEU ...
 A G C C T A A A C G C C A T A G A C A T A T C A C G C C T A ...
 5410 5420 5430 ...
 ... THR ASN HIS ARG THR PRO ARG ALA ASP SER
 ... A C C A A C C A T C G G A C G C C T A G G C T G A C A G T
 5440 5450 5460 ...

FIG. 8W

ASN ASN THR LEU TYR SER THR SER LEU ILE ...
 A A T A A C A C T T A T A C A G T A C C T C A T T G A T T ...
 5470 5490 ...

... TYR TYR PRO ASN ALA THR ARG TYR TYR LEU
 ... T A T T A C C C A A T G C C A C A C G C T A T T A T C T T
 5510 5520 ...

...
 LEU GLY ALA ASP PHE TYR ASP GLU LYS VAL ...
 T T G G G G C A G A C T T A T G A T G A A A A G T G ...
 5530 5540 5550 ...

... PRO GLN ASP PRO SER ASP SER TYR GLN ARG 60/73
 ... C C A C A A G A C C C A T C T G A C A G T T A T C A A C G C
 5560 5570 5580 ...

...
 ARG GLY ILE ARG THR ALA TRP GLY GLN GLU ...
 C G T G G C A T A C G C A C A G C G T G G G G C A A G A A ...
 5590 5600 5610 ...

... TRP ALA GLY GLY LEU SER SER ARG ALA GLN
 ... T G G G C G G G T G G T C T T C A A G C C G T G C C C A A
 5620 5630 5640 ...

...
 ILE SER ILE ASN LYS ARG HIS TYR GLN GLY ...
 A T C A G C A T C A A C A A A C G C C A T T A C C A A G G G ...
 5650 5660 5670 ...

... ALA ASN LEU THR SER GLY GLY GLN ILE ARG
 ... G C A A A C C T A A C C A G C G G T G G A C A A A T T C G C
 5680 5690 5700 ...

FIG. 8X

HIS ASP LYS GLN MET GLN ALA SER LEU SER ...
 C A T G A T A A C A G A T G C A A G C G T C T T A T C G ...
 5710 5720 5730...
 ... LEU TRP HIS ARG ASP ILE HIS LYS TRP GLY
 ... C T T T G G C A C A G A G A C A T T C A C A T G G G C
 5740 5750 5760
 ...
 ILE THR PRO ARG LEU THR ILE SER THR ASN ...
 A T C A C G C C A C C G C T G A C C A T C A G C A C A A C ...
 5770 5780 5790...
 ... ILE ASN LYS SER ASN ASP ILE LYS ALA ASN
 ... A T C A A T A A A A G C A A T G A C A T C A A G G C A A T
 5800 5810 5820
 ...
 TYR HIS LYS ASN GLN MET PHE VAL GLU PHE ...
 T A T C A C A A A A T C A A A T G T T G T G A G T T T ...
 5830 5840 5850...
 ... SER ARG ILE PHE ***
 ... A G T C G C A T T T G A T G G G A T A A G C A C G C C
 5860 5870 5880
 ...
 C T A C T T T G T T T G T A A A A A T G T G C C A ...
 5890 5900 5910...
 ... T C A T A G A C A A T C A A G A A A A T C A A G A A
 5920 5930 5940
 ...

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AAAAAGATACAAATTATTGATAATTGTT...
 5950
 5970...
 ... ATTGTTATGTTATTTCAATGTTAA
 5980
 5990
 6000

TTGCCCCATTGTCCTATCATAAATGCAAT...
 6020
 6030...
 ... TTATCAAAATGCTCAAAATAAATACGCCAAAT
 6040
 6050
 ...

GCAACATTGTCAGCAATGCCAAATAGGCCAAATC...
 6070
 6080
 6090...
 ... AACAGACTTTAGATAAAATACCATCACCC
 6110
 6120
 ...

tlpB
 MET LYS HIS ILE ...
 CATTCAAGGATTTATGAAACACATTC...
 6130
 6140
 6150...
 ... PRO LEU THR LEU CYS VAL ALA ILE SER A
 ... CTTTAAACCAACACTGTTGCGCAATCTCG
 6170
 6180

FIG.8Z

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LA VAL LEU LEU THR ALA CYS GLY GLY SER ...
C C G T C T T A T T A A C C G C T T G T G G C A G T G...
6190 ...
...GLY GLY SER ASN PRO ALA PRO THR PRO I
... G T G G T T C A A A T C C A C C T G C T C C T C G C C A
6200 ...
...
6220 ...
6230 ...
6240 ...

LE PRO ASN ALA SER GLY SER GLY ASN THR ...
T T C C A A A T G C T A G C G G T T C A G G T A A T A C T G...
6250 ...
...GLY ASN THR GLY ASN ALA GLY GLY THR ASP A
... G C A A C A C T G G T A A T G C T G G C G G T A C T G A T A 63/73
...
6260 ...
...
6270 ...
...
...
6280 ...
6290 ...
...
6300 ...

SN THR ALA ASN ALA GLY ASN THR GLY GLY ...
A T A C A G C C A A T G C A G G T A A T A C A G G C G G T A...
6310 ...
...THR ASN SER GLY THR GLY SER ALA ASN THR P
... C A A A C T C T G G T A C A G G C A G T G C C A A C A C
6320 ...
...
6330 ...
...
6340 ...
6350 ...
6360 ...

RO GLU PRO LYS TYR GLN ASP VAL PRO THR ...
C A G A G C C A A A T A T C A A G A T G T A C C A A C T G...
6370 ...
...GLU LYS ASN GLU LYS ASP LYS VAL SER SER I
... A G A A A A T G A A A A G A T A A A G T T C A T C C A
6380 ...
...
6400 ...
6410 ...
6420 ...

FIG.8A'

LE GIN GLU PRO ALA MET GLY TYR GLY MET ...
 T T C A A G A A C C T G C C A T G G G T T A T G G C A T G G ...
 6430 6440 6450 ...
 ... ALA LEU SER LYS ILE ASN LEU HIS ASN ARG G
 ... C T T T G A G T A A A T T A A T C T A C A C C G A C
 6460 6470 6480 6490 6500 6510 ...
 ...
 LN ASP THR PRO LEU ASP GLU LYS ASN ILE ...
 A A G A C A C G C C A T T A G A T G A A A A A T A T C A ...
 6520 6530 6540 6550 6560 6570 ...
 ... ILE THR LEU ASP GLY LYS GLN VAL ALA G
 ... T T A C C T T A G A C G G T A A A A A C A A G T T G C A G
 6580 6590 6600 ...
 ...
 LU GLY LYS LYS SER PRO LEU PRO PHE SER ...
 A A G G T A A A A A T C G C C A T T G C C A T T C G T ...
 6610 6620 6630 ...
 ... LEU ASP VAL GLU ASN LYS LEU LEU ASP GLY T
 ... T A G A T G T A G A A A T T A A A T T G C T T G A T G G C T
 6640 6650 6660 ...
 ...
 YR ILE ALA LYS MET ASN VAL ALA ASP LYS ...
 A T A T A G C A A A A T G A A T G T A G C G G A T A A A A ...
 6670 6680 6690 ...
 ... ASN ALA ILE ASP ARG ILE LYS LYS GLY A
 ... A T G C C A T T G G T G A C A G A A T T A A G A A T T A A G G T A
 6700 6710 6720 ...

FIG. 8B.

SN LYS GLU ILE SER ASP GLU GLU LEU ALA ...
 AT AAA GAA ATC TCC GAT GAA CTT GCC A...
 6670 ...
 6680 ... LYS GLN ILE LYS GLU ALA VAL ARG LYS SER H
 ... A CAA ATC AAA GAA GCT GTG C G T A A A A G C C
 6720 ...
 ...
 IS GLU PHE GIN GIN VAL LEU SER SER LEU ...
 AT GAG TTT CAG CAA GTA TTA TCA TCA C T G G ...
 6730 ...
 6740 ... GLU ASN LYS ILE PHE HIS SER ASN ASP GLY T
 ... A A A C A A A A T T T C A T T C A A T G A C G G A A
 6770 ...
 ...
 HR THR LYS ALA THR THR ARG ASP LEU LYS ...
 C A C C A A G C A A C C A C A C G A G A T T A A A T ...
 6790 ...
 6800 ... TYR VAL ASP TYR GLY TYR TYR ILE ALA ASN A
 ... A T G T T G A T T A T G G T T A C T A C T A C T A C T G
 6820 ...
 ...
 SP GLY ASN TYR LEU THR VAL LYS THR ASP ...
 AT GGC AATTA TCTAA CCGTC A A A C A G A C A ...
 6850 ...
 6860 ... LYS LEU TRP ASN LEU GLY PRO VAL GLY GLY V
 ... A C T T T G G A A T T A G G C C C T G T G G T G
 6890 ...
 ...

FIG.8C'

AL	PHE	TYR	ASN	GLY	THR	THR	ALA	LYS	...	
T G T T T A T A A T G G C A C A A C G A C C G C C A A G...	6910	6920	6930...	6940	6950	6960	6970	6980	6990...	
YS	GLY	HIS	TRP	ASP	PHE	MET	THR	ASP	VAL	...
A A G G A C A T T G G A C T T A T G A C C G A T G T T G...	6970	6980	6990...	7000	7010	7020	7030	7040	7050...	
YS	GLU	ASN	SER	GLN	ALA	GLY	TRP	TYR	TYR	...
A A G A A A C T C T C A A G C A G G C T G G T A T T A T G...	7030	7040	7050...	7060	7070	7080	7090	7100	7110...	
EU	LEU	THR	LYS	GLU	ASP	SER	ALA	PRO	ASP	...
T A T T A A C T A A A G A A G A C T C T G C C C T G A T G...	7090	7100	7110...	7120	7130	7140	7150	7160	7170...	

FIG. 8D.

LU PHE THR VAL ASN PHE LYS GLU LYS LYS ...
 AGTTACCTGTTAATTTAAGGAAAGAAAT...
 7150
 ...LEU THR GLY LYS LEU PHE SER ASN LEU GLN A
 ...TAAACAGGTTAACGCTGTATAGTAACTAACAG
 7160
 ...
 7170...
 SP ARG HIS LYS GLY ASN VAL THR LYS THR ...
 ACCGCCATTAAGGGCAATGTTACAAACCG...
 7210
 ...GLU ARG TYR ASP ILE ASP AIA ASN ILE HIS G
 ...AACGCTATGACATCGCATGCGAACATATC
 7220
 ...
 7230...
 LY ASN ARG PHE ARG GLY SER ALA THR ALA ...
 GCAACCGCTTCCGTGGCAGTGGCACCGCAAA...
 7270
 ...SER ASN LYS ASN ASP THR SER LYS HIS PRO P
 ...GCAATTAAATGACACAAAGCAAAACACCC
 7280
 ...
 7290...
 HE THR SER ASP ALA ASN ARG LEU GLU ...
 TTACCAAGTGAATGCCAACAAATAGGCCTAGAAG...
 7330
 ...GLY GLY PHE TYR GLY PRO LYS GLY GLU L
 ...GTTGGTTTATGGGCCAACAAAGCGAGGAGC
 7340
 ...
 7350...
 7360
 ...
 7370
 ...
 7380

FIG. 8E'

EU	ALA	GLY	LYS	PHE	LEU	THR	ASN	ASP	ASN	...
T G G C A G G T A A A T T C T T A A C C A A T G A C A A C A . . .										
7390	7400	7410 . . .								
...LYS	LEU	PHE	GLY	VAL	PHE	GLY	ALA	LYS	ARG	G
... A A C T C T T T G G C G T C T T G G T G C T A A A C C G A G										
7420	7430	7440	7450	7460	7470 . . .					
LU	SER	LYS	ALA	GLU	GLU	LYS	THR	GLU	ALA	...
A G A G T A A A G C T G A G G A A A A A C C G A A G C C A . . .										
7450	7460	7470 . . .								
...ILE	LEU	ASP	ALA	TYR	ALA	LEU	GLY	THR	PHE	A
... T C T T A G A T G C C T A T G C A C T T G G A C A T T T A										
7480	7490	7500	7510	7520	7530 . . .					
SN	THR	SER	ASN	ALA	THR	THR	PHE	THR	PRO	...
A T A C A A G T A A C G C A A C C A A C C A T T C A C C C A T . . .										
7510	7520	7530 . . .								
...PHE	THR	GLU	LYS	GLN	LEU	ASP	ASN	PHE	GLY	A
... T T A C C G A A A A A C A A C T G G A T A A C T T G G C A										
7540	7550	7560	7570	7580	7590 . . .					
SN	ALA	LYS	LYS	LEU	VAL	LEU	GLY	SER	THR	...
A T G C C A A A A A T T G G T C T T A G G T T C T A C C G . . .										
7570	7580	7590 . . .								
...VAL	ILE	ASP	LEU	VAL	PRO	THR	ASP	ALA	THR	L
... T C A T T G A T T G G C C T A C T G A T G C C A C C A										
7600	7610	7620	...							

FIG. 8F

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FIG.8G'

YR ILE THR GLY LYS ASP THR GLY THR GLY GLY ...
A C A T C A C A G G A A A G G A C A C A G G A C A G G C A ...
7870 7880 7890 ...
... THR GLY LYS SER PHE THR ASP ALA GIN ASP V
... C A G G A A A A A G C T T T A C C G A T G C C C C A A G A T G
7900 7910 7920 ...
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AL ALA ASP PHE ASP ILE ASP PHE GLY ASN ...
T T G C T G A T T G A C A T T G A T T G A T T G G A A A T A A ...
7930 7940 7950 ...
... LYS SER VAL SER GLY LYS LEU ILE THR LYS G
... A A T C A G T C A G C G G T A A A C T T A T C A C C A A A G
7960 7970 7980 ...

LY ARG GLN ASP PRO VAL PHE SER ILE THR ...
G C C G C C A A G A C C C T G T A T T A G C A T C A C A G ...
7990 8000 8010 ...
... GLY GLN ILE ALA GLY ASN GLY TRP ILE GLY T
... G T C A A A T C G C A G G C A A T G G C T G G A C A G G G A
8020 8030 8040 ...

HR ALA SER THR THR LYS ALA ASP ALA GLY ...
C A G C C A G C A C C A C C A A G C G G A C G G A G G A G ...
8050 8060 8070 ...
... GLY TYR LYS ILE ASP SER SER THR GLY L
... G C T A C A A G A T A G A T T C T A G C A G C A G T A C A G G C A
8080 8090 8100 ...

FIG.8H'

YS	SER	ILE	ALA	ILE	LYS	ASP	ALA	ASN	VAL	...	
AA	T	C	C	A	T	C	G	C	C	A	...
8110	8120	8130	8140	8150	8160						
LU	MET	GLY	GLY	SER	PHE	THR	HIS	ASN	ALA	...	
AG	A	T	G	G	G	G	T	C	A	...	
8170	8180	8190	8200	8210	8220						
HR	LYS	ARG	GIN	GIN	GLU	VAL	LYS	***			
CA	AA	AA	AG	AC	AA	CA	AG	AT	AA	...	
8230	8240	8250	8260								

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FIG. 9A

Alignment of *M. catarrhalis* ORF3 proteins

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FIG. 9B

ADFYDEKVPQDPSDSYQRRGIRTANGQEWAGGLSSRAQISINKRHYQGAN
.....E.....
410 420 430 440 450
.....
LTSGQIRHDQMQASLSLWHRDIHKWGITPRLTISTINKSNDIKANYH
.....Q.....
460 470 480 490 500
.....
KNQMFVEFSRIF*
.....*.....
510
.....
4223
Q8